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Sequence Listing was accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=8; day=28; hr=10; min=10; sec=1; ms=415;]

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Application No: 10586111

Version No: 2.1

Input Set:

Output Set:

Started: 2008-08-28 10:05:09.924

Finished: 2008-08-28 10:05:12.068

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 144 ms

Total Warnings: 9

Total Errors: 0

No. of SeqIDs Defined: 9

Actual SeqID Count: 9

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<110> Fraunhofer Gesellschaft zur Forderung der angewandten
Forschung e.V.

<120> Immunokinases

<130> 3581.10-US-01

<140> 10/586,111
<141> 2006-07-14

<150> PCT/EP05/50131
<151> 2005-01-13

<150> 04000847.6
<151> 2004-01-16

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<170> PatentIn version 3.5

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<211> 1785
<212> DNA
<213> Artificial Sequence

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open reading frame (ORF)

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<220>
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<223>   immunoglobulin kappa chain leader sequence
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aat atg gag acg ttc aaa cag cag aag gtg gag gac ttt tat gat att 144
Asn Met Glu Thr Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile
35 40 45

gga gag gag ctg ggc agt ggc cag ttt gcc atc gtg aag aag tgc cgg	192
Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg	
50 55 60	
 gag aag agc acg ggg ctg gag tat gca gcc aag ttc att aag aag agg	240
Glu Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg	
65 70 75 80	
 cag agc cgg gcc agc cgt cgg ggc gtg tgc cgg gag gaa atc gag cgg	288
Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg	
85 90 95	
 gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg	336
Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu	
100 105 110	
 cac gac gtc tat gag aac cgc acc gac gtg gtg ctc atc ctt gag cta	384
His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu	
115 120 125	
 gtg tcc gga gga gaa ctg ttt gat ttc ctg gcc cag aag gag tgc tta	432
Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu	
130 135 140	
 agt gag gag gaa gcc acc agc ttc att aag cag atc ctg gat ggg gtg	480
Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val	
145 150 155 160	
 aat tac ctt cac aca aag aaa att gct cac ttt gat ctc aag cca gaa	528
Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu	
165 170 175	
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Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu	
180 185 190	
 att gac ttt ggc ctg gct cac gaa ata gaa gat gga gtt gaa ttt aaa	624
Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys	
195 200 205	
 aac att ttt ggg aca cct gaa ttt gtt gct cca gaa atc gtg aac tat	672
Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr	
210 215 220	
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Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr	
225 230 235 240	
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Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln	
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 gaa acc ctg gca aat atc act gct gtg agt tac gac ttt gat gag gaa	816
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu	
260 265 270	
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Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu	
275 280 285	
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Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg	
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His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala	
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Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser Gly Tyr	
340 345 350	
acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct gga cag	1104
Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln	
355 360 365	
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Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp	
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tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac aaa tcc	1200
Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser	
385 390 395 400	
tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag gat tct	1248
Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser	
405 410 415	
gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg ggg ttt	1296
Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe	
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cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc	1344
Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly	
435 440 445	
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Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu	
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Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr	
465 470 475 480	
ttg agc tgc aag gcc agt gag aat gtg gat tct ttt gtt tcc tgg tat	1488
Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr	
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caa cag aaa cca ggc cag tct cct aaa ctg ctg ata tac ggg gcc tcc	1536
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Gln Ser Arg Ala Ser Arg Arg Gly Val Cys Arg Glu Glu Ile Glu Arg
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Glu Val Ser Ile Leu Arg Gln Val Leu His Pro Asn Ile Ile Thr Leu
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His Asp Val Tyr Glu Asn Arg Thr Asp Val Val Leu Ile Leu Glu Leu
115 120 125

Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu
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Ser Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val
145 150 155 160

Asn Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu
165 170 175

Asn Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu
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Ile Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys
195 200 205

Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr
210 215 220

Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr
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Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln
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Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu
260 265 270

Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu
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Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg
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His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala

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His Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Gly Asp Ala Ala						
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Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln						
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Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr Thr Asp						
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Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser						
385		390		395		400
Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser						
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Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp Gly Phe						
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Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly						
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Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg Val Thr						
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Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser Trp Tyr						
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Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly Ala Ser						
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Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly Ser Gly						
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Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala						
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 Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu
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 cag gag tca ggg act gaa ctg gca aag cct ggg gcc gca gtg aag atg 144
 Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met
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 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp
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 Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn
 65 70 75 80

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Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala	
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aca ttg act gca gac aaa tcc tcc agc aca gcc tac atg caa ctg cgc	336
Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg	
100 105 110	
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Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr	
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Thr Gln Thr Thr Trp Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val	
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Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
145 150 155 160	
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Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met	
165 170 175	
tca gtc gga gag agg gtc acc ttg agc tgc aag gcc agt gag aat gtg	576
Ser Val Gly Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val	
180 185 190	
gat tct ttt gtt tcc tgg tat caa cag aaa cca ggc cag tct cct aaa	624
Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	